(c) amplifying DNA encoding MN present in the cDNA prepared in step (b); and

(d) detecting the presence of any resulting amplified DNA, the presence of such amplified DNA being diagnostic for renal carcinoma.

39. The method of claim 38, wherein in step (c) amplification of DNA encoding MN is effected by a polymerase chain reaction utilizing at least two oligonucleotide primers.

B2 CON'T.

40. The method of claim 39, wherein each of the primers is capable of specifically hybridizing with DNA encoding MN.

41. The method of claim 39, wherein the primers comprise oligonucleotides that are effective to amplify a segment of the MN cDNA.

42. The method of claim 41 wherein said MN cDNA has the nucleotide sequence of SEQ ID NO: 1.

43. The method of claim 42 wherein one of said primers comprises the nucleotide sequence of nucleotide 404 to nucleotide

423 of Figure 1A-1B and of SEQ ID NO: 1, and the other primer is complementary to nucleotides 789 to 770 of Figure 1A-1B and of SEQ ID NO: 1.

44. The method of claim 38, wherein the presence of any amplified DNA in step (d) is detected using a labeled MN nucleic acid probe which specifically hybridizes with MN nucleic acids encoding a MN protein or MN polypeptide, which MN protein or MN polypeptide has an amino acid sequence of or from SEQ ID NO: 2.

45. The method of claim 44, wherein the labeled probe is radiolabeled.

46. The method of claim 39 wherein each of said primers is an isolated and purified MN nucleic acid, which has a length of from 16 nucleotides to 50 nucleotides, and comprises a nucleotide sequence which is selected from the group consisting of: nucleotide sequences that specifically hybridize to SEQ ID NO: 1 or to the complement of SEQ ID NO: 1; and

wherein an appropriate pair of primers is selected for effective amplification.

47. The method of claim 46 wherein said nucleotide sequence specifically hybridizes to a MN nucleotide sequence contained in any of the plasmids A4a, XE1 and XE3, which were deposited at the American Type Culture Collection in the United States of America under the respective ATCC Nos. 97199, 97200 and 97198.

B2 CONT.

48. A method of screening for preneoplastic/neoplastic disease associated with abnormal MN gene expression comprising:

(a) determining whether abnormal MN gene expression is present in a vertebrate using a nucleic acid based assay on a sample from said vertebrate; and

(b) if abnormal MN gene expression is determined to be present in said vertebrate, determining that said vertebrate has a significant risk of having preneoplastic/neoplastic disease;

wherein said MN gene encodes an MN protein that is encoded by a nucleic acid having a nucleotide sequence selected from the group consisting of:

(a) SEQ ID NO: 1;

(b) nucleotide sequences that hybridize under stringent conditions to complement of SEQ ID NO: 1; and

(c) nucleotide sequences that differ from SEQ ID NO: 1 or from the nucleotide sequences of (b) in codon sequence due to the degeneracy of the genetic code.

49. The method of claim 48 wherein said MN protein is encoded by SEQ ID NO: 1.

50. The method of claim 49 wherein said vertebrate is a mammal.

51. The method of claim 49 wherein said vertebrate is a human.

52. The method of claim 51 wherein said nucleic acid based assay is a polymerase chain reaction based assay.

53. The method of claim 51 wherein detecting abnormal MN gene expression comprises:

(a) obtaining mRNA from said sample from said human; and

(b) detecting the presence of mRNA that is complementary to MN cDNA in the mRNA obtained from step (b), or

quantitating any mRNA that is complementary to MN cDNA in the mRNA obtained from step (b);

wherein the presence of mRNA complementary to MN cDNA in said mRNA obtained in step (a), or an abnormal level of mRNA complementary to MN cDNA in said mRNA obtained in step (a), indicates the presence of preneoplastic/neoplastic disease in said human.

B2 CON

54. The method of claim 51 wherein abnormal MN gene expression is detected by:

(a) obtaining mRNA from a sample from said human;

(b) preparing cDNA from the mRNA from step (a);

(c) amplifying any DNA encoding a MN protein or a MN polypeptide that is present in the cDNA prepared in step (b); and

(d) detecting the presence of any resulting amplified DNA, or quantitating any resulting amplified DNA, wherein the presence of such amplified DNA or an abnormal level of said amplified DNA indicates the presence of preneoplastic/neoplastic disease in said human.

55. The method of claim 54, wherein the step (c) amplification of DNA is effected by a polymerase chain reaction utilizing at least two oligonucleotide primers.

56. The method of claim 55 wherein each of the primers is capable of specifically hybridizing with DNA that encodes MN protein.

57. The method of claim 56 wherein said DNA that encodes MN protein has the nucleotide sequence of SEQ ID NO: 1.

58. The method of claim 57 wherein one of said primers has the nucleotide sequence of nucleotide 404 to nucleotide 423 of Figure 1A-1B or of SEQ ID NO: 1, and the other primer is complementary to nucleotide 789 to nucleotide 770 of Figure 1A-1B or of SEQ ID NO: 1.

59. The method of claim 54, wherein the presence of any amplified DNA in step (d) is detected using a labeled MN nucleic acid probe which specifically hybridizes with any amplified MN DNA.

60. The method of claim 59, wherein the labeled probe is radiolabeled.

61. The method of claim 60 wherein the labeled probe is radiolabeled with ^{32}P.

62. The method of claim 53 wherein said sample is selected from the group consisting of tissue sections, tissue extracts, tissue smears, whole cells, cell lysates, exfoliated cells, cell extracts, and body fluids.

B2 cont.

63. The method according to claim 62 wherein said body fluid is selected from the group consisting of blood, serum, plasma, urine, semen, breast exudate, saliva, sputum, tears, mucous, fecal suspensions, gastric secretions, bile, lymph, cytosols, ascites, pleural effusions, amniotic fluid, bladder washes, bronchioalveolar lavages and cerebrospinal fluid.

64. The method according to claim 63 wherein said body fluid is selected from the group consisting of blood, serum and plasma.

65. The method according to claim 64 wherein said body fluid is blood.

66. The method of claim 54 wherein said preneoplastic/neoplastic disease associated with abnormal MN gene expression is selected from the group consisting of mammary, urinary tract, bladder, kidney, ovarian, uterine, cervical,

endometrial, squamous cell, adenosquamous cell, vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic, testicular, brain, head and neck, mesodermal, sarcomal, stomach, spleen, gastrointestinal, esophageal, and colon preneoplastic/neoplastic diseases.

67. The method of claim 66 wherein said neoplastic disease is renal carcinoma.

REMARKS

The Specification has been amended to up-date the status of a claimed priority application which has been issued as a patent.

Claims 1, 2, 6, 13-17, 24, 25 and 35-37 were cancelled, and new claims 38-67 were added to point out with more particularity and clarity the subject matter regarded by the Applicants as their invention, and to serve to provoke an interference with the McKiernan et al. '098 patent. Applicants respectfully submit that the new claims are supported throughout the application.